

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/325,603

DATE: 07/08/1999
TIME: 11:11:34

INPUT SET: S32473.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Svendsen, Allan
6 Bisgrd-Frantzen, Henrik
7 Borchert, Torben Vedel
8
9 (ii) TITLE OF INVENTION: Å-Amylase Mutants
10
11 (iii) NUMBER OF SEQUENCES: 13
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Novo Nordisk of North America, Inc.
15 (B) STREET: 405 Lexington Avenue, 64th Floor
16 (C) CITY: New York
17 (D) STATE: New York
18 (E) COUNTRY: United States of America
19 (F) ZIP: 10174-6401
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 09/325,603
29 (B) FILING DATE:
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/600,908
34 (B) FILING DATE:
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Green, Reza
38 (B) REGISTRATION NUMBER: 38,475
39 (C) REFERENCE/DOCKET NUMBER: 4394.204-US
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 212-867-0123
43 (B) TELEFAX: 212-878-9655
44
45
46 (2) INFORMATION FOR SEQ ID NO:1:

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 1920 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
53
54      (ii) MOLECULE TYPE: DNA (genomic)
55
56      (ix) FEATURE:
57          (A) NAME/KEY: CDS
58          (B) LOCATION: 334..1869
59
60      (ix) FEATURE:
61          (A) NAME/KEY: sig_peptide
62          (B) LOCATION: 334..420
63
64      (ix) FEATURE:
65          (A) NAME/KEY: mat_peptide
66          (B) LOCATION: 421..1869
67
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70      CGGAAGATTG GAAGTACAAA AATAAGCAAA AGATTGTCAA TCATGTCATG AGCCATGCGG      60
71
72      GAGACGGAAA AATCGTCTTA ATGCACGATA TTTATGCAAC GTTCGCAGAT GCTGCTGAAG      120
73
74      AGATTATTAA AAAGCTGAAA GCAAAAAGGCT ATCAATTGGT AACTGTATCT CAGCTTGAAG      180
75
76      AAGTGAAGAA GCAGAGAGGC TATTGAATAA ATGAGTAGAA GCGCCATATC GGCGCTTTTC      240
77
78      TTTTGGAAGA AAATATAGGG AAAATGGTAC TTGTTAAAAA TTCGGAATAT TTATACAACA      300
79
80      TCATATGTTT CACATTGAAA GGGGAGGAGA ATC ATG AAA CAA CAA AAA CGG CTT      354
81                                     Met Lys Gln Gln Lys Arg Leu
82                                     -29                               -25
83
84      TAC GCC CGA TTG CTG ACG CTG TTA TTT GCG CTC ATC TTC TTG CTG CCT      402
85      Tyr Ala Arg Leu Leu Thr Leu Leu Phe Ala Leu Ile Phe Leu Leu Pro
86      -20                               -15                               -10
87
88      CAT TCT GCA GCA GCG GCG GCA AAT CTT AAT GGG ACG CTG ATG CAG TAT      450
89      His Ser Ala Ala Ala Ala Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr
90      -5                               1                               5                               10
91
92      TTT GAA TGG TAC ATG CCC AAT GAC GGC CAA CAT TGG AGG CGT TTG CAA      498
93      Phe Glu Trp Tyr Met Pro Asn Asp Gly Gln His Trp Arg Arg Leu Gln
94      15                               20                               25
95
96      AAC GAC TCG GCA TAT TTG GCT GAA CAC GGT ATT ACT GCC GTC TGG ATT      546
97      Asn Asp Ser Ala Tyr Leu Ala Glu His Gly Ile Thr Ala Val Trp Ile
98      30                               35                               40
99
  
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100	CCC	CCG	GCA	TAT	AAG	GGA	ACG	AGC	CAA	GCG	GAT	GTG	GGC	TAC	GGT	GCT	594
101	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	
102			45					50					55				
103																	
104	TAC	GAC	CTT	TAT	GAT	TTA	GGG	GAG	TTT	CAT	CAA	AAA	GGG	ACG	GTT	CGG	642
105	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe	His	Gln	Lys	Gly	Thr	Val	Arg	
106		60					65					70					
107																	
108	ACA	AAG	TAC	GGC	ACA	AAA	GGA	GAG	CTG	CAA	TCT	GCG	ATC	AAA	AGT	CTT	690
109	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu	Leu	Gln	Ser	Ala	Ile	Lys	Ser	Leu	
110		75				80					85					90	
111																	
112	CAT	TCC	CGC	GAC	ATT	AAC	GTT	TAC	GGG	GAT	GTG	GTC	ATC	AAC	CAC	AAA	738
113	His	Ser	Arg	Asp	Ile	Asn	Val	Tyr	Gly	Asp	Val	Val	Ile	Asn	His	Lys	
114					95					100					105		
115																	
116	GGC	GGC	GCT	GAT	GCG	ACC	GAA	GAT	GTA	ACC	GCG	GTT	GAA	GTC	GAT	CCC	786
117	Gly	Gly	Ala	Asp	Ala	Thr	Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asp	Pro	
118				110					115				120				
119																	
120	GCT	GAC	CGC	AAC	CGC	GTA	ATT	TCA	GGA	GAA	CAC	CTA	ATT	AAA	GCC	TGG	834
121	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	Gly	Glu	His	Leu	Ile	Lys	Ala	Trp	
122			125					130					135				
123																	
124	ACA	CAT	TTT	CAT	TTT	CCG	GGG	CGC	GGC	AGC	ACA	TAC	AGC	GAT	TTT	AAA	882
125	Thr	His	Phe	His	Phe	Pro	Gly	Arg	Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	
126		140					145					150					
127																	
128	TGG	CAT	TGG	TAC	CAT	TTT	GAC	GGA	ACC	GAT	TGG	GAC	GAG	TCC	CGA	AAG	930
129	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	
130		155				160					165					170	
131																	
132	CTG	AAC	CGC	ATC	TAT	AAG	TTT	CAA	GGA	AAG	GCT	TGG	GAT	TGG	GAA	GTT	978
133	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	
134					175					180					185		
135																	
136	TCC	AAT	GAA	AAC	GGC	AAC	TAT	GAT	TAT	TTG	ATG	TAT	GCC	GAC	ATC	GAT	1026
137	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	
138				190					195				200				
139																	
140	TAT	GAC	CAT	CCT	GAT	GTC	GCA	GCA	GAA	ATT	AAG	AGA	TGG	GGC	ACT	TGG	1074
141	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	
142			205					210					215				
143																	
144	TAT	GCC	AAT	GAA	CTG	CAA	TTG	GAC	GGT	TTC	CGT	CTT	GAT	GCT	GTC	AAA	1122
145	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	
146		220					225					230					
147																	
148	CAC	ATT	AAA	TTT	TCT	TTT	TTG	CGG	GAT	TGG	GTT	AAT	CAT	GTC	AGG	GAA	1170
149	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp	Trp	Val	Asn	His	Val	Arg	Glu	
150		235				240					245					250	
151																	
152	AAA	ACG	GGG	AAG	GAA	ATG	TTT	ACG	GTA	GCT	GAA	TAT	TGG	CAG	AAT	GAC	1218

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153	Lys Thr Gly Lys Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp	
154	255 260 265	
155		
156	TTG GGC GCG CTG GAA AAC TAT TTG AAC AAA ACA AAT TTT AAT CAT TCA	1266
157	Leu Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Phe Asn His Ser	
158	270 275 280	
159		
160	GTG TTT GAC GTG CCG CTT CAT TAT CAG TTC CAT GCT GCA TCG ACA CAG	1314
161	Val Phe Asp Val Pro Leu His Tyr Gln Phe His Ala Ala Ser Thr Gln	
162	285 290 295	
163		
164	GGA GGC GGC TAT GAT ATG AGG AAA TTG CTG AAC GGT ACG GTC GTT TCC	1362
165	Gly Gly Gly Tyr Asp Met Arg Lys Leu Leu Asn Gly Thr Val Val Ser	
166	300 305 310	
167		
168	AAG CAT CCG TTG AAA TCG GTT ACA TTT GTC GAT AAC CAT GAT ACA CAG	1410
169	Lys His Pro Leu Lys Ser Val Thr Phe Val Asp Asn His Asp Thr Gln	
170	315 320 325 330	
171		
172	CCG GGG CAA TCG CTT GAG TCG ACT GTC CAA ACA TGG TTT AAG CCG CTT	1458
173	Pro Gly Gln Ser Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu	
174	335 340 345	
175		
176	GCT TAC GCT TTT ATT CTC ACA AGG GAA TCT GGA TAC CCT CAG GTT TTC	1506
177	Ala Tyr Ala Phe Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe	
178	350 355 360	
179		
180	TAC GGG GAT ATG TAC GGG ACG AAA GGA GAC TCC CAG CGC GAA ATT CCT	1554
181	Tyr Gly Asp Met Tyr Gly Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro	
182	365 370 375	
183		
184	GCC TTG AAA CAC AAA ATT GAA CCG ATC TTA AAA GCG AGA AAA CAG TAT	1602
185	Ala Leu Lys His Lys Ile Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr	
186	380 385 390	
187		
188	GCG TAC GGA GCA CAG CAT GAT TAT TTC GAC CAC CAT GAC ATT GTC GGC	1650
189	Ala Tyr Gly Ala Gln His Asp Tyr Phe Asp His His Asp Ile Val Gly	
190	395 400 405 410	
191		
192	TGG ACA AGG GAA GGC GAC AGC TCG GTT GCA AAT TCA GGT TTG GCG GCA	1698
193	Trp Thr Arg Glu Gly Asp Ser Ser Val Ala Asn Ser Gly Leu Ala Ala	
194	415 420 425	
195		
196	TTA ATA ACA GAC GGA CCC GGT GGG GCA AAG CGA ATG TAT GTC GGC CGG	1746
197	Leu Ile Thr Asp Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg	
198	430 435 440	
199		
200	CAA AAC GCC GGT GAG ACA TGG CAT GAC ATT ACC GGA AAC CGT TCG GAG	1794
201	Gln Asn Ala Gly Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu	
202	445 450 455	
203		
204	CCG GTT GTC ATC AAT TCG GAA GGC TGG GGA GAG TTT CAC GTA AAC GGC	1842
205	Pro Val Val Ile Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly	

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206          460          465          470
207
208 GGG TCG GTT TCA ATT TAT GTT CAA AGA TAGAAGAGCA GAGAGGACGG      1889
209 Gly Ser Val Ser Ile Tyr Val Gln Arg
210 475          480
211
212 ATTCCTGAA GGAAATCCGT TTTTATT T      1920
213
214
215 (2) INFORMATION FOR SEQ ID NO:2:
216
217     (i) SEQUENCE CHARACTERISTICS:
218         (A) LENGTH: 512 amino acids
219         (B) TYPE: amino acid
220         (D) TOPOLOGY: linear
221
222     (ii) MOLECULE TYPE: protein
223
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
225
226 Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
227 -29          -25          -20          -15
228
229 Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
230          -10          -5          1
231
232 Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly
233     5          10          15
234
235 Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His
236 20          25          30          35
237
238 Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln
239          40          45          50
240
241 Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
242          55          60          65
243
244 His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu
245          70          75          80
246
247 Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly
248 85          90          95
249
250 Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val
251 100          105          110          115
252
253 Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly
254          120          125          130
255
256 Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly
257          135          140          145
258

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text